IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of ) Group Art Unit: 1812

Dan L. Eaton et al. ) Examiner: Unassigned

Serial No. 08/423,194 )

Filed: 18 April 1995 )

For: MPL LIGAND )

## CERTIFICATE RE: SEQUENCE LISTING

BOX SEQUENCE
Honorable Commissioner of Patents
  and Trademarks
Washington, D.C. 20231

Sir:

I hereby state that the Sequence Listing submitted herewith is submitted in paper copy and a computer-readable diskette, and that the content of the paper and computer readable copies are the same.

Respectfully submitted,

GENENTECH, INC.

Date: September 8, 1995

By: _____
Daryl B. Winter
Reg. No. 32,637

460 Pt. San Bruno Blvd.
So. San Francisco, CA 94080-4990
Phone: (415) 225-1249
Fax: (415) 952-9881

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Eaton, Dan L.
                de Sauvage, Frederic J.

(ii) TITLE OF INVENTION: MPL LIGAND

(iii) NUMBER OF SEQUENCES: 77

(iv) CORRESPONDENCE ADDRESS:
    (A) ADDRESSEE: Genentech, Inc.
    (B) STREET: 460 Point San Bruno Blvd
    (C) CITY: South San Francisco
    (D) STATE: California
    (E) COUNTRY: USA
    (F) ZIP: 94080

(v) COMPUTER READABLE FORM:
    (A) MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
    (B) COMPUTER: IBM PC compatible
    (C) OPERATING SYSTEM: PC-DOS/MS-DOS
    (D) SOFTWARE: patin (Genentech)

(vi) CURRENT APPLICATION DATA:
    (A) APPLICATION NUMBER: 08/423194
    (B) FILING DATE: 18-APR-1995
    (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
    (A) APPLICATION NUMBER: 08/249376
    (B) FILING DATE: 25-MAY-1994

(vii) PRIOR APPLICATION DATA:
    (A) APPLICATION NUMBER: 08/223263
    (B) FILING DATE: 04-APR-1994

(vii) PRIOR APPLICATION DATA:
    (A) APPLICATION NUMBER: 08/196689
    (B) FILING DATE: 15-FEB-1994

(vii) PRIOR APPLICATION DATA:
    (A) APPLICATION NUMBER: 08/185607
    (B) FILING DATE: 21-JAN-1994

(vii) PRIOR APPLICATION DATA:
    (A) APPLICATION NUMBER: 08/176553
    (B) FILING DATE: 03-JAN-1994

(viii) ATTORNEY/AGENT INFORMATION:
    (A) NAME: Winter, Daryl B.

(2)  INFORMATION FOR SEQ ID NO:1:

    (i)  SEQUENCE CHARACTERISTICS:
        (A)  LENGTH: 353 amino acids
        (B)  TYPE: amino acid
        (D)  TOPOLOGY: linear

    (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
Met Glu Leu Thr Glu Leu Leu Leu Val Val Met Leu Leu Leu Thr
-21 -20              -15                 -10

Ala Arg Leu Thr Leu Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu
    -5               1               5

Arg Val Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser
10              15              20

Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val
25              30              35

Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln
40              45              50

Met Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly Ala Val Thr Leu
55              60              65

Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Gly Pro Thr
70              75              80

Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu
85              90              95

Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu Pro Pro
100             105             110

Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe Leu
115             120             125

Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu
130             135             140

Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala Pro Pro Thr Thr
145             150             155
```

```
Ala Val Pro Ser Arg Thr Ser Leu Val Leu Thr Leu Asn Glu Leu
160             165             170

Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr Asn Phe Thr Ala Ser
175             180             185

Ala Arg Thr Thr Gly Ser Gly Leu Leu Lys Trp Gln Gln Gly Phe
190             195             200

Arg Ala Lys Ile Pro Gly Leu Leu Asn Gln Thr Ser Arg Ser Leu
205             210             215

Asp Gln Ile Pro Gly Tyr Leu Asn Arg Ile His Glu Leu Leu Asn
220             225             230

Gly Thr Arg Gly Leu Phe Pro Gly Pro Ser Arg Arg Thr Leu Gly
235             240             245

Ala Pro Asp Ile Ser Ser Gly Thr Ser Asp Thr Gly Ser Leu Pro
250             255             260

Pro Asn Leu Gln Pro Gly Tyr Ser Pro Ser Pro Thr His Pro Pro
265             270             275

Thr Gly Gln Tyr Thr Leu Phe Pro Leu Pro Pro Thr Leu Pro Thr
280             285             290

Pro Val Val Gln Leu His Pro Leu Leu Pro Asp Pro Ser Ala Pro
295             300             305

Thr Pro Thr Pro Thr Ser Pro Leu Leu Asn Thr Ser Tyr Thr His
310             315             320

Ser Gln Asn Leu Ser Gln Glu Gly
325             330     332
```

(2) INFORMATION FOR SEQ ID NO:2:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 1795 bases
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
TCTTCCTACC CATCTGCTCC CCAGAGGGCT GCCTGCTGTG CACTTGGGTC 50

CTGGAGCCCT TCTCCACCCG GATAGATTCC TCACCCTTGG CCCGCCTTTG 100
```

CCCCACCCTA CTCTGCCCAG AAGTGCAAGA GCCTAAGCCG CCTCCATGGC 150

CCCAGGAAGG ATTCAGGGGA GAGGCCCCAA ACAGGGAGCC ACGCCAGCCA 200

GACACCCCGG CCAGAATGGA GCTGACTGAA TTGCTCCTCG TGGTCATGCT 250

TCTCCTAACT GCAAGGCTAA CGCTGTCCAG CCCGGCTCCT CCTGCTTGTG 300

ACCTCCGAGT CCTCAGTAAA CTGCTTCGTG ACTCCCATGT CCTTCACAGC 350

AGACTGAGCC AGTGCCCAGA GGTTCACCCT TTGCCTACAC CTGTCCTGCT 400

GCCTGCTGTG GACTTTAGCT TGGGAGAATG GAAAACCCAG ATGGAGGAGA 450

CCAAGGCACA GGACATTCTG GGAGCAGTGA CCCTTCTGCT GGAGGGAGTG 500

ATGGCAGCAC GGGGACAACT GGGACCCACT TGCCTCTCAT CCCTCCTGGG 550

GCAGCTTTCT GGACAGGTCC GTCTCCTCCT TGGGGCCCTG CAGAGCCTCC 600

TTGGAACCCA GCTTCCTCCA CAGGGCAGGA CCACAGCTCA CAAGGATCCC 650

AATGCCATCT TCCTGAGCTT CCAACACCTG CTCCGAGGAA AGGTGCGTTT 700

CCTGATGCTT GTAGGAGGGT CCACCCTCTG CGTCAGGCGG GCCCCACCCA 750

CCACAGCTGT CCCCAGCAGA ACCTCTCTAG TCCTCACACT GAACGAGCTC 800

CCAAACAGGA CTTCTGGATT GTTGGAGACA AACTTCACTG CCTCAGCCAG 850

AACTACTGGC TCTGGGCTTC TGAAGTGGCA GCAGGGATTC AGAGCCAAGA 900

TTCCTGGTCT GCTGAACCAA ACCTCCAGGT CCCTGGACCA AATCCCCGGA 950

TACCTGAACA GGATACACGA ACTCTTGAAT GGAACTCGTG GACTCTTTCC 1000

-107-

TGGACCCTCA CGCAGGACCC TAGGAGCCCC GGACATTTCC TCAGGAACAT 1050

CAGACACAGG CTCCCTGCCA CCCAACCTCC AGCCTGGATA TTCTCCTTCC 1100

CCAACCCATC CTCCTACTGG ACAGTATACG CTCTTCCCTC TTCCACCCAC 1150

CTTGCCCACC CCTGTGGTCC AGCTCCACCC CCTGCTTCCT GACCCTTCTG 1200

CTCCAACGCC CACCCCTACC AGCCCTCTTC TAAACACATC CTACACCCAC 1250

TCCCAGAATC TGTCTCAGGA AGGGTAAGGT TCTCAGACAC TGCCGACATC 1300

AGCATTGTCT CATGTACAGC TCCCTTCCCT GCAGGGCGCC CCTGGGAGAC 1350

AACTGGACAA GATTTCCTAC TTTCTCCTGA AACCCAAAGC CCTGGTAAAA 1400

GGGATACACA GGACTGAAAA GGGAATCATT TTTCACTGTA CATTATAAAC 1450

CTTCAGAAGC TATTTTTTTA AGCTATCAGC AATACTCATC AGAGCAGCTA 1500

GCTCTTTGGT CTATTTTCTG CAGAAATTTG CAACTCACTG ATTCTCTACA 1550

TGCTCTTTTT CTGTGATAAC TCTGCAAAGG CCTGGGCTGG CCTGGCAGTT 1600

GAACAGAGGG AGAGACTAAC CTTGAGTCAG AAAACAGAGA AAGGGTAATT 1650

TCCTTTGCTT CAAATTCAAG GCCTTCCAAC GCCCCATCC CCTTTACTAT 1700

CATTCTCAGT GGGACTCTGA TCCCATATTC TTAACAGATC TTTACTCTTG 1750

AGAAATGAAT AAGCTTTCTC TCAGAAAAAA AAAAAAAAA AAAAA 1795

(2) INFORMATION FOR SEQ ID NO:3:

-108-

(i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 42 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Leu Leu Leu Val Val Met Leu Leu Leu Thr Ala Arg Leu Thr Leu
-16 -15              -10                  -5

Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys
      1            5                10

Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu
 15              20                  25  26

(2) INFORMATION FOR SEQ ID NO:4:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 390 bases
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAATTCCTGG AATACCAGCT GACAATGATT TCCTCCTCAT CTTTCAACCT 50

CACCTCTCCT CATCTAAGAA TTGCTCCTCG TGGTCATGCT TCTCCTAACT 100

GCAAGGCTAA CGCTGTCCAG CCCGGCTCCT CCTGCTTGTG ACCTCCGAGT 150

CCTCAGTAAA CTGCTTCGTG ACTCCCATGT CCTTCACAGC AGACTGGTGA 200

GAACTCCCAA CATTATCCCC TTTATCCGCG TAACTGGTAA GACACCCATA 250

CTCCCAGGAA GACACCATCA CTTCCTCTAA CTCCTTGACC CAATGACTAT 300

TCTTCCCATA TTGTCCCCAC CTACTGATCA CACTCTCTGA CAAGAATTAT 350

TCTTCACAAT ACAGCCCGCA TTTAAAAGCT CTCGTCTAGA 390

(2) INFORMATION FOR SEQ ID NO:5:

   (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 390 bases
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTTAAGGACC TTATGGTCGA CTGTTACTAA AGGAGGAGTA GAAAGTTGGA 50

GTGGAGAGGA GTAGATTCTT AACGAGGAGC ACCAGTACGA AGAGGATTGA 100

CGTTCCGATT GCGACAGGTC GGGCCGAGGA GGACGAACAC TGGAGGCTCA 150

GGAGTCATTT GACGAAGCAC TGAGGGTACA GGAAGTGTCG TCTGACCACT 200

CTTGAGGGTT GTAATAGGGG AAATAGGCGC ATTGACCATT CTGTGGGTAT 250

GAGGGTCCTT CTGTGGTAGT GAAGGAGATT GAGGAACTGG GTTACTGATA 300

AGAAGGGTAT AACAGGGGTG GATGACTAGT GTGAGAGACT GTTCTTAATA 350

AGAAGTGTTA TGTCGGGCGT AAATTTTCGA GAGCAGATCT 390

(2) INFORMATION FOR SEQ ID NO:6:

   (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 332 amino acids
      (B) TYPE: amino acid
      (D) TOPOLOGY: linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu
1               5                  10                  15

Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro
                20                  25                  30

-110-

```
        Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp
                        35          40              45

      Phe Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala
 5                      50              55                  60

      Gln Asp Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met
                        65              70                  75

10    Ala Ala Arg Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu
                        80              85                  90

      Gly Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln
                        95              100                 105
15
      Ser Leu Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala
                        110             115                 120

      His Lys Asp Pro Asn Ala Ile Phe Leu Ser Phe Gln His Leu Leu
20                      125             130                 135

      Arg Gly Lys Val Arg Phe Leu Met Leu Val Gly Gly Ser Thr Leu
                        140             145                 150

      Cys Val Arg Arg Ala Pro Pro Thr Thr Ala Val Pro Ser Arg Thr
                        155             160                 165

      Ser Leu Val Leu Thr Leu Asn Glu Leu Pro Asn Arg Thr Ser Gly
                        170             175                 180
30
      Leu Leu Glu Thr Asn Phe Thr Ala Ser Ala Arg Thr Thr Gly Ser
                        185             190                 195

      Gly Leu Leu Lys Trp Gln Gln Gly Phe Arg Ala Lys Ile Pro Gly
35                      200             205                 210

      Leu Leu Asn Gln Thr Ser Arg Ser Leu Asp Gln Ile Pro Gly Tyr
                        215             220                 225

40    Leu Asn Arg Ile His Glu Leu Leu Asn Gly Thr Arg Gly Leu Phe
                        230             235                 240

      Pro Gly Pro Ser Arg Arg Thr Leu Gly Ala Pro Asp Ile Ser Ser
                        245             250                 255
45
      Gly Thr Ser Asp Thr Gly Ser Leu Pro Pro Asn Leu Gln Pro Gly
                        260             265                 270

      Tyr Ser Pro Ser Pro Thr His Pro Pro Thr Gly Gln Tyr Thr Leu
50                      275             280                 285
```

-111-

```
Phe Pro Leu Pro Pro Thr Leu Pro Thr Pro Val Val Gln Leu His
            290              295               300

Pro Leu Leu Pro Asp Pro Ser Ala Pro Thr Pro Thr Pro Thr Ser
            305              310               315

Pro Leu Leu Asn Thr Ser Tyr Thr His Ser Gln Asn Leu Ser Gln
            320              325               330

Glu Gly
332
```

(2) INFORMATION FOR SEQ ID NO:7:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 166 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr
1                5                10               15

Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala
            20               25               30

Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys
            35               40               45

Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala
            50               55               60

Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu
            65               70               75

Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro
            80               85               90

Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu
            95               100              105

Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser
            110              115              120

Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala
            125              130              135

Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg
            140              145              150
```

-112-

```
Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
                155                 160                 165

Arg
166

(2) INFORMATION FOR SEQ ID NO:8:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 328 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu
  1             5                10                15

Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro
             20                25                30

Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp
             35                40                45

Phe Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala
             50                55                60

Gln Asp Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met
             65                70                75

Ala Ala Arg Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu
             80                85                90

Gly Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln
             95               100               105

Ser Leu Leu Gly Thr Gln Gly Arg Thr Thr Ala His Lys Asp Pro
            110               115               120

Asn Ala Ile Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val
            125               130               135

Arg Phe Leu Met Leu Val Gly Gly Ser Thr Leu Cys Val Arg Arg
            140               145               150

Ala Pro Pro Thr Thr Ala Val Pro Ser Arg Thr Ser Leu Val Leu
            155               160               165

Thr Leu Asn Glu Leu Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr
            170               175               180
```

-113-

```
Asn Phe Thr Ala Ser Ala Arg Thr Thr Gly Ser Gly Leu Leu Lys
                185                 190                 195

Trp Gln Gln Gly Phe Arg Ala Lys Ile Pro Gly Leu Leu Asn Gln
                200                 205                 210

Thr Ser Arg Ser Leu Asp Gln Ile Pro Gly Tyr Leu Asn Arg Ile
                215                 220                 225

His Glu Leu Leu Asn Gly Thr Arg Gly Leu Phe Pro Gly Pro Ser
                230                 235                 240

Arg Arg Thr Leu Gly Ala Pro Asp Ile Ser Ser Gly Thr Ser Asp
                245                 250                 255

Thr Gly Ser Leu Pro Pro Asn Leu Gln Pro Gly Tyr Ser Pro Ser
                260                 265                 270

Pro Thr His Pro Pro Thr Gly Gln Tyr Thr Leu Phe Pro Leu Pro
                275                 280                 285

Pro Thr Leu Pro Thr Pro Val Val Gln Leu His Pro Leu Leu Pro
                290                 295                 300

Asp Pro Ser Ala Pro Thr Pro Thr Pro Thr Ser Pro Leu Leu Asn
                305                 310                 315

Thr Ser Tyr Thr His Ser Gln Asn Leu Ser Gln Glu Gly
                320                 325             328
```

(2) INFORMATION FOR SEQ ID NO:9:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 265 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```
Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu
  1                 5                 10                  15

Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro
                20                  25                  30

Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp
                35                  40                  45

Phe Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala
                50                  55                  60
```

```
            Gln Asp Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met
                            65              70              75

        Ala Ala Arg Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu
5                           80              85              90

        Gly Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln
                            95              100             105

10      Ser Leu Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala
                            110             115             120

        His Lys Asp Pro Asn Ala Ile Phe Leu Ser Phe Gln His Leu Leu
15                          125             130             135

        Arg Gly Lys Asp Phe Trp Ile Val Gly Asp Lys Leu His Cys Leu
                            140             145             150

20      Ser Gln Asn Tyr Trp Leu Trp Ala Ser Glu Val Ala Ala Gly Ile
                            155             160             165

        Gln Ser Gln Asp Ser Trp Ser Ala Glu Pro Asn Leu Gln Val Pro
                            170             175             180

25      Gly Pro Asn Pro Arg Ile Pro Glu Gln Asp Thr Arg Thr Leu Glu
                            185             190             195

30      Trp Asn Ser Trp Thr Leu Ser Trp Thr Leu Thr Gln Asp Pro Arg
                            200             205             210

        Ser Pro Gly His Phe Leu Arg Asn Ile Arg His Arg Leu Pro Ala
                            215             220             225

35      Thr Gln Pro Pro Ala Trp Ile Phe Ser Phe Pro Asn Pro Ser Ser
                            230             235             240

        Tyr Trp Thr Val Tyr Ala Leu Pro Ser Ser Thr His Leu Ala His
                            245             250             255

40      Pro Cys Gly Pro Ala Pro Pro Pro Ala Ser
                            260             265
```

(2) INFORMATION FOR SEQ ID NO:10:

45          (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 261 amino acids
                (B) TYPE: amino acid
                (D) TOPOLOGY: linear

50          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

-115-

```
Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu
  1               5               10              15

Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro
 5                  20              25                  30

Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp
10                  35              40                  45

Phe Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala
10                  50              55                  60

Gln Asp Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met
15                  65              70                  75

Ala Ala Arg Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu
                80              85                  90

Gly Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln
20                  95              100                 105

Ser Leu Leu Gly Thr Gln Gly Arg Thr Thr Ala His Lys Asp Pro
                110             115                 120

Asn Ala Ile Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys Asp
25                  125             130                 135

Phe Trp Ile Val Gly Asp Lys Leu His Cys Leu Ser Gln Asn Tyr
                140             145                 150

Trp Leu Trp Ala Ser Glu Val Ala Ala Gly Ile Gln Ser Gln Asp
30                  155             160                 165

Ser Trp Ser Ala Glu Pro Asn Leu Gln Val Pro Gly Pro Asn Pro
35                  170             175                 180

Arg Ile Pro Glu Gln Asp Thr Arg Thr Leu Glu Trp Asn Ser Trp
                185             190                 195

Thr Leu Ser Trp Thr Leu Thr Gln Asp Pro Arg Ser Pro Gly His
40                  200             205                 210

Phe Leu Arg Asn Ile Arg His Arg Leu Pro Ala Thr Gln Pro Pro
                215             220                 225
45
Ala Trp Ile Phe Ser Phe Pro Asn Pro Ser Ser Tyr Trp Thr Val
                230             235                 240

Tyr Ala Leu Pro Ser Ser Thr His Leu Ala His Pro Cys Gly Pro
50                  245             250                 255
```

-116-

Ala Pro Pro Pro Ala Ser
                  260 261

(2) INFORMATION FOR SEQ ID NO:11:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1443 bases
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAGTCCTTGG CCCACCTCTC TCCCACCCGA CTCTGCCGAA AGAAGCACAG 50

AAGCTCAAGC CGCCTCCATG GCCCCAGGAA AGATTCAGGG GAGAGGCCCC 100

ATACAGGGAG CCACTTCAGT TAGACACCCT GGCCAGAATG GAGCTGACTG 150

ATTTGCTCCT GGCGGCCATG CTTCTTGCAG TGGCAAGACT AACTCTGTCC 200

AGCCCCGTAG CTCCTGCCTG TGACCCCAGA CTCCTAAATA AACTGCTGCG 250

TGACTCCCAC CTCCTTCACA GCCGACTGAG TCAGTGTCCC GACGTCGACC 300

CTTTGTCTAT CCCTGTTCTG CTGCCTGCTG TGGACTTTAG CCTGGGAGAA 350

TGGAAAACCC AGACGGAACA GAGCAAGGCA CAGGACATTC TAGGGGCAGT 400

GTCCCTTCTA CTGGAGGGAG TGATGGCAGC ACGAGCACAG TTGGAACCCT 450

CCTGCCTCTC ATCCCTCCTG GGACAGCTTT CTGGGCAGGT TCGCCTCCTC 500

TTGGGGGCCC TGCAGGGCCT CCTAGGAACC CAGGGCAGGA CCACAGCTCA 550

CAAGGACCCC AATGCCCTCT TCTTGAGCTT GCAACAACTG CTTCGGGGAA 600

AGGTGCGCTT CCTGCTTCTG GTAGAAGGTC CCACCCTCTG TGTCAGACGG 650

-117-

ACCCTGCCAA CCACAGCTGT CCCAAGCAGT ACTTCTCAAC TCCTCACACT 700

AAACAAGTTC CCAAACAGGA CTTCTGGATT GTTGGAGACG AACTTCAGTG 750

TCACAGCCAG AACTGCTGGC CCTGGACTTC TGAGCAGGCT TCAGGGATTC 800

AGAGTCAAGA TTACTCCTGG TCAGCTAAAT CAAACCTCCA GGTCCCCAGT 850

CCAAATCTCT GGATACCTGA ACAGGACACA CGGACCTGTG AATGGAACTC 900

ATGGGCTCTT TGCTGGAACC TCACTTCAGA CCCTGGAAGC CTCAGACATC 950

TCGCCCGGAG CTTTCAACAA AGGCTCCCTG GCATTCAACC TCCAGGGTGG 1000

ACTTCCTCCT TCTCCAAGCC TTGCTCCTGA TGGACACACA CCCTTCCCTC 1050

CTTCACCTGC CTTGCCCACC ACCGATGGAT CTCCACCCCA GCTCCACCCC 1100

CTGTTTCCTG ACCCTTCCAC CACCATGCCT AACTCTACCG CCCCTCATCC 1150

AGTCACAATG TACCCTCATC CCAGGAATTT GTCTCAGGAA ACATAGCGCG 1200

GGCACTGGCC CAGTGAGCGT CTGCAGCTTC TCTCGGGGAC AAGCTTCCCC 1250

AGGAAGGCTG AGAGGCAGCT GCATCTGCTC CAGATGTTCT GCTTTCACCT 1300

AAAAGGCCCT GGGGAAGGGA TACACAGCAC TGGAGATTGT AAAATTTTAG 1350

GAGCTATTTT TTTTTAACCT ATCAGCAATA TTCATCAGAG CAGCTAGCGA 1400

TCTTTGGTCT ATTTTCGGTA TAAATTTGAA AATCACTAAT TCT 1443


(2) INFORMATION FOR SEQ ID NO:12:

    (i) SEQUENCE CHARACTERISTICS:

-118-

(A) LENGTH: 352 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```
Met Glu Leu Thr Asp Leu Leu Leu Ala Ala Met Leu Leu Ala Val
-21 -20              -15             -10

Ala Arg Leu Thr Leu Ser Ser Pro Val Ala Pro Ala Cys Asp Pro
    -5               1               5

Arg Leu Leu Asn Lys Leu Leu Arg Asp Ser His Leu Leu His Ser
10              15              20

Arg Leu Ser Gln Cys Pro Asp Val Asp Pro Leu Ser Ile Pro Val
25              30              35

Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln
40              45              50

Thr Glu Gln Ser Lys Ala Gln Asp Ile Leu Gly Ala Val Ser Leu
55              60              65

Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Glu Pro Ser
70          75              80

Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu
85              90              95

Leu Leu Gly Ala Leu Gln Gly Leu Leu Gly Thr Gln Gly Arg Thr
100             105             110

Thr Ala His Lys Asp Pro Asn Ala Leu Phe Leu Ser Leu Gln Gln
115             120             125

Leu Leu Arg Gly Lys Val Arg Phe Leu Leu Leu Val Glu Gly Pro
130             135             140

Thr Leu Cys Val Arg Arg Thr Leu Pro Thr Thr Ala Val Pro Ser
145             150             155

Ser Thr Ser Gln Leu Leu Thr Leu Asn Lys Phe Pro Asn Arg Thr
160             165             170

Ser Gly Leu Leu Glu Thr Asn Phe Ser Val Thr Ala Arg Thr Ala
175             180             185

Gly Pro Gly Leu Leu Ser Arg Leu Gln Gly Phe Arg Val Lys Ile
190             195             200
```

-119-

```
Thr Pro Gly Gln Leu Asn Gln Thr Ser Arg Ser Pro Val Gln Ile
205             210             215

Ser Gly Tyr Leu Asn Arg Thr His Gly Pro Val Asn Gly Thr His
220             225             230

Gly Leu Phe Ala Gly Thr Ser Leu Gln Thr Leu Glu Ala Ser Asp
235             240             245

Ile Ser Pro Gly Ala Phe Asn Lys Gly Ser Leu Ala Phe Asn Leu
250             255             260

Gln Gly Gly Leu Pro Pro Ser Pro Ser Leu Ala Pro Asp Gly His
265             270             275

Thr Pro Phe Pro Pro Ser Pro Ala Leu Pro Thr Thr His Gly Ser
280             285             290

Pro Pro Gln Leu His Pro Leu Phe Pro Asp Pro Ser Thr Thr Met
295             300             305

Pro Asn Ser Thr Ala Pro His Pro Val Thr Met Tyr Pro His Pro
310             315             320

Arg Asn Leu Ser Gln Glu Thr
325             330 331
```

(2) INFORMATION FOR SEQ ID NO:13:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1536 bases
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAGTCCTTGG CCCACCTCTC TCCCACCCGA CTCTGCCGAA AGAAGCACAG 50

AAGCTCAAGC CGCCTCCATG GCCCCAGGAA AGATTCAGGG GAGAGGCCCC 100

ATACAGGGAG CCACTTCAGT TAGACACCCT GGCCAGAATG GAGCTGACTG 150

ATTTGCTCCT GGCGGCCATG CTTCTTGCAG TGGCAAGACT AACTCTGTCC 200

AGCCCCGTAG CTCCTGCCTG TGACCCCAGA CTCCTAAATA AACTGCTGCG 250
```

-120-

TGACTCCCAC CTCCTTCACA GCCGACTGAG TCAGTGTCCC GACGTCGACC 300

CTTTGTCTAT CCCTGTTCTG CTGCCTGCTG TGGACTTTAG CCTGGGAGAA 350

TGGAAAACCC AGACGGAACA GAGCAAGGCA CAGGACATTC TAGGGGCAGT 400

GTCCCTTCTA CTGGAGGGAG TGATGGCAGC ACGAGGACAG TTGGAACCCT 450

CCTGCCTCTC ATCCTCCTG GGACAGCTTT CTGGGCAGGT TCGCCTCCTC 500

TTGGGGGCCC TGCAGGGCCT CCTAGGAACC CAGCTTCCTC TACAGGGCAG 550

GACCACAGCT CACAAGGACC CCAATGCCCT CTTCTTGAGC TTGCAACAAC 600

TGCTTCGGGG AAAGGTGCGC TTCCTGCTTC TGGTAGAAGG TCCCACCCTC 650

TGTGTCAGAC GGACCCTGCC AACCACAGCT GTCCCAAGCA GTACTTCTCA 700

ACTCCTCACA CTAAACAAGT TCCCAAACAG GACTTCTGGA TTGTTGGAGA 750

CGAACTTCAG TGTCACAGCC AGAACTGCTG GCCCTGGACT TCTGAGCAGG 800

CTTCAGGGAT TCAGAGTCAA GATTACTCCT GGTCAGCTAA ATCAAACCTC 850

CAGGTCCCCA GTCCAAATCT CTGGATACCT GAACAGGACA CACGGACCTG 900

TGAATGGAAC TCATGGGCTC TTTGCTGGAA CCTCACTTCA GACCCTGGAA 950

GCCTCAGACA TCTCGCCCGG AGCTTTCAAC AAAGGCTCCC TGGCATTCAA 1000

CCTCCAGGGT GGACTTCCTC CTTCTCCAAG CCTTGCTCCT GATGGACACA 1050

CACCCTTCCC TCCTTCACCT GCCTTGCCCA CCACCCATGG ATCTCCACCC 1100

CAGCTCCACC CCCTGTTTCC TGACCCTTCC ACCACCATGC CTAACTCTAC 1150

-121-

CGCCCCTCAT CCAGTCACAA TGTACCCTCA TCCCAGGAAT TGTCTCAGG 1200

AAACATAGCG CGGGCACTGG CCCAGTGAGC GTCTGCAGCT TCTCTCGGGG 1250

ACAAGCTTCC CCAGGAAGGC TGAGAGGCAG CTGCATCTGC TCCAGATGTT 1300

CTGCTTTCAC GTAAAAGGCC CTGGGGAAGG GATACACAGC ACTGGAGATT 1350

GTAAAATTTT AGGAGCTATT TTTTTTTAAC CTATCAGCAA TATTCATCAG 1400

AGCAGCTAGC GATCTTTGGT CTATTTTCGG TATAAATTTG AAAATCACTA 1450

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1500

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAA 1536

(2) INFORMATION FOR SEQ ID NO:14:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 356 amino acids
       (B) TYPE: amino acid
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Glu Leu Thr Asp Leu Leu Leu Ala Ala Met Leu Leu Ala Val
-21 -20                -15                -10

Ala Arg Leu Thr Leu Ser Ser Pro Val Ala Pro Ala Cys Asp Pro
    -5                1                5

Arg Leu Leu Asn Lys Leu Leu Arg Asp Ser His Leu Leu His Ser
10                15                20

Arg Leu Ser Gln Cys Pro Asp Val Asp Pro Leu Ser Ile Pro Val
25                30                35

Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln
40                45                50

Thr Glu Gln Ser Lys Ala Gln Asp Ile Leu Gly Ala Val Ser Leu
55                60                65

-122-

Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Glu Pro Ser  
70      75      80  

Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu  
85      90      95  

Leu Leu Gly Ala Leu Gln Gly Leu Leu Gly Thr Gln Leu Pro Leu  
100     105     110  

Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Leu Phe Leu  
115     120     125  

Ser Leu Gln Gln Leu Leu Arg Gly Lys Val Arg Phe Leu Leu Leu  
130     135     140  

Val Glu Gly Pro Thr Leu Cys Val Arg Arg Thr Leu Pro Thr Thr  
145     150     155  

Ala Val Pro Ser Ser Thr Ser Gln Leu Leu Thr Leu Asn Lys Phe  
160     165     170  

Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr Asn Phe Ser Val Thr  
175     180     185  

Ala Arg Thr Ala Gly Pro Gly Leu Leu Ser Arg Leu Gln Gly Phe  
190     195     200  

Arg Val Lys Ile Thr Pro Gly Gln Leu Asn Gln Thr Ser Arg Ser  
205     210     215  

Pro Val Gln Ile Ser Gly Tyr Leu Asn Arg Thr His Gly Pro Val  
220     225     230  

Asn Gly Thr His Gly Leu Phe Ala Gly Thr Ser Leu Gln Thr Leu  
235     240     245  

Glu Ala Ser Asp Ile Ser Pro Gly Ala Phe Asn Lys Gly Ser Leu  
250     255     260  

Ala Phe Asn Leu Gln Gly Gly Leu Pro Pro Ser Pro Ser Leu Ala  
265     270     275  

Pro Asp Gly His Thr Pro Phe Pro Pro Ser Pro Ala Leu Pro Thr  
280     285     290  

Thr His Gly Ser Pro Pro Gln Leu His Pro Leu Phe Pro Asp Pro  
295     300     305  

Ser Thr Thr Met Pro Asn Ser Thr Ala Pro His Pro Val Thr Met  
310     315     320

Tyr Pro His Pro Arg Asn Leu Ser Gln Glu Thr
325                 330                 335

(2) INFORMATION FOR SEQ ID NO:15:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 241 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Ser Pro Val Ala Pro Ala Cys Asp Pro Arg Leu Leu Asn Lys Leu
 1               5                  10               15

Leu Arg Asp Ser His Leu Leu His Ser Arg Leu Ser Gln Cys Pro
                20                  25               30

Asp Val Asp Pro Leu Ser Ile Pro Val Leu Leu Pro Ala Val Asp
                35                  40               45

Phe Ser Leu Gly Glu Trp Lys Thr Gln Thr Glu Gln Ser Lys Ala
                50                  55               60

Gln Asp Ile Leu Gly Ala Val Ser Leu Leu Leu Glu Gly Val Met
                65                  70               75

Ala Ala Arg Gly Gln Leu Glu Pro Ser Cys Leu Ser Ser Leu Leu
                80                  85               90

Gly Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln
                95                  100              105

Gly Leu Leu Gly Thr Gln Leu Pro Leu Gln Gly Arg Thr Thr Ala
                110                 115              120

His Lys Asp Pro Asn Ala Leu Phe Leu Ser Leu Gln Gln Leu Leu
                125                 130              135

Arg Gly Lys Asp Phe Trp Ile Val Gly Asp Glu Leu Gln Cys His
                140                 145              150

Ser Gln Asn Cys Trp Pro Trp Thr Ser Glu Gln Ala Ser Gly Ile
                155                 160              165

Gln Ser Gln Asp Tyr Ser Trp Ser Ala Lys Ser Asn Leu Gln Val
                170                 175              180

Pro Ser Pro Asn Leu Trp Ile Pro Glu Gln Asp Thr Arg Thr Cys
                185                 190              195

-124-

Glu Trp Asn Ser Trp Ala Leu Cys Trp Asn Leu Thr Ser Asp Pro
          200                    205                    210

Gly Ser Leu Arg His Leu Ala Arg Ser Phe Gln Gln Arg Leu Pro
          215                    220                    225

Gly Ile Gln Pro Pro Gly Trp Thr Ser Ser Phe Ser Lys Pro Cys
          230                    235                    240

Ser
241

(2) INFORMATION FOR SEQ ID NO:16:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 335 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ser Pro Val Ala Pro Ala Cys Asp Pro Arg Leu Leu Asn Lys Leu
  1             5                    10                    15

Leu Arg Asp Ser His Leu Leu His Ser Arg Leu Ser Gln Cys Pro
          20                    25                    30

Asp Val Asp Pro Leu Ser Ile Pro Val Leu Leu Pro Ala Val Asp
          35                    40                    45

Phe Ser Leu Gly Glu Trp Lys Thr Gln Thr Glu Gln Ser Lys Ala
          50                    55                    60

Gln Asp Ile Leu Gly Ala Val Ser Leu Leu Leu Glu Gly Val Met
          65                    70                    75

Ala Ala Arg Gly Gln Leu Glu Pro Ser Cys Leu Ser Ser Leu Leu
          80                    85                    90

Gly Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln
          95                    100                    105

Gly Leu Leu Gly Thr Gln Leu Pro Leu Gln Gly Arg Thr Thr Ala
          110                    115                    120

His Lys Asp Pro Asn Ala Leu Phe Leu Ser Leu Gln Gln Leu Leu
          125                    130                    135

Arg Gly Lys Val Arg Phe Leu Leu Leu Val Glu Gly Pro Thr Leu
          140                    145                    150

-125-

```
Cys Val Arg Arg Thr Leu Pro Thr Thr Ala Val Pro Ser Ser Thr
                155             160             165

Ser Gln Leu Leu Thr Leu Asn Lys Phe Pro Asn Arg Thr Ser Gly
                170             175             180

Leu Leu Glu Thr Asn Phe Ser Val Thr Ala Arg Thr Ala Gly Pro
                185             190             195

Gly Leu Leu Ser Arg Leu Gln Gly Phe Arg Val Lys Ile Thr Pro
                200             205             210

Gly Gln Leu Asn Gln Thr Ser Arg Ser Pro Val Gln Ile Ser Gly
                215             220             225

Tyr Leu Asn Arg Thr His Gly Pro Val Asn Gly Thr His Gly Leu
                230             235             240

Phe Ala Gly Thr Ser Leu Gln Thr Leu Glu Ala Ser Asp Ile Ser
                245             250             255

Pro Gly Ala Phe Asn Lys Gly Ser Leu Ala Phe Asn Leu Gln Gly
                260             265             270

Gly Leu Pro Pro Ser Pro Ser Leu Ala Pro Asp Gly His Thr Pro
                275             280             285

Phe Pro Pro Ser Pro Ala Leu Pro Thr Thr His Gly Ser Pro Pro.
                290             295             300

Gln Leu His Pro Leu Phe Pro Asp Pro Ser Thr Thr Met Pro Asn
                305             310             315

Ser Thr Ala Pro His Pro Val Thr Met Tyr Pro His Pro Arg Asn
                320             325             330

Leu Ser Gln Glu Thr
                335
```

(2) INFORMATION FOR SEQ ID NO:17:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 332 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```
Ser Pro Ala Pro Pro Ala Cys Asp Pro Arg Leu Leu Asn Lys Leu
  1           5                   10                  15
```

-126-

```
        Leu Arg Asp Ser His Val Leu His Gly Arg Leu Ser Gln Cys Pro
                     20                  25                  30
  5     Asp Ile Asn Pro Leu Ser Thr Pro Val Leu Leu Pro Ala Val Asp
                     35                  40                  45
        Phe Thr Leu Gly Glu Trp Lys Thr Gln Thr Glu Gln Thr Lys Ala
                     50                  55                  60
 10     Gln Asp Val Leu Gly Ala Thr Thr Leu Leu Leu Glu Ala Val Met
                     65                  70                  75
        Thr Ala Arg Gly Gln Val Gly Pro Pro Cys Leu Ser Ser Leu Leu
                     80                  85                  90
 15     Val Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln
                     95                 100                 105
 20     Asp Leu Leu Gly Met Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala
                    110                 115                 120
        His Lys Asp Pro Ser Ala Ile Phe Leu Asn Phe Gln Gln Leu Leu
                    125                 130                 135
 25     Arg Gly Lys Val Arg Phe Leu Leu Leu Val Val Gly Pro Ser Leu
                    140                 145                 150
        Cys Ala Lys Arg Ala Pro Pro Ala Ile Ala Val Pro Ser Ser Thr
                    155                 160                 165
 30     Ser Pro Phe His Thr Leu Asn Lys Leu Pro Asn Arg Thr Ser Gly
                    170                 175                 180
        Leu Leu Glu Thr Asn Ser Ser Ile Ser Ala Arg Thr Thr Gly Ser
                    185                 190                 195
 35     Gly Phe Leu Lys Arg Leu Gln Ala Phe Arg Ala Lys Ile Pro Gly
                    200                 205                 210
 40     Leu Leu Asn Gln Thr Ser Arg Ser Leu Asp Gln Ile Pro Gly His
                    215                 220                 225
        Gln Asn Gly Thr His Gly Pro Leu Ser Gly Ile His Gly Leu Phe
                    230                 235                 240
 45     Pro Gly Pro Gln Pro Gly Ala Leu Gly Ala Pro Asp Ile Pro Pro
                    245                 250                 255
        Ala Thr Ser Gly Met Gly Ser Arg Pro Thr Tyr Leu Gln Pro Gly
 50                 260                 265                 270
```

```
Glu Ser Pro Ser Pro Ala His Pro Ser Pro Gly Arg Tyr Thr Leu
                275             280                     285

Phe Ser Pro Ser Pro Thr Ser Pro Ser Pro Thr Val Gln Leu Gln
                290             295                     300

Pro Leu Leu Pro Asp Pro Ser Ala Ile Thr Pro Asn Ser Thr Ser
                305             310                     315

Pro Leu Leu Phe Ala Ala His Pro His Phe Gln Asn Leu Ser Gln
                320             325                     330

Glu Glu
    332
```

(2) INFORMATION FOR SEQ ID NO:18:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1026 bases
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```
AGCCCGGCTC CTCCTGCCTG TGACCCCCGA CTCCTAAATA AACTGCTTCG 50

TGACTCCCAT GTCCTTCACG GCAGACTGAG CCAGTGCCCA GACATTAACC 100

CTTTGTCCAC ACCTGTCCTG CTGCCTGCTG TGGACTTCAC CTTGGGAGAA 150

TGGAAAACCC AGACGGAGCA GACAAAGGCA CAGGATGTCC TGGGAGCCAC 200

AACCCTTCTG CTGGAGGCAG TGATGACAGC ACGGGGACAA GTGGGACCCC 250

CTTGCCTCTC ATCCCTGCTG GTGCAGCTTT CTGGACAGGT TCGCCTCCTC 300

CTCGGGGCCC TGCAGGACCT CCTTGGAATG CAGCTTCCTC CACAGGGAAG 350

GACCACAGCT CACAAGGATC CCAGTGCCAT CTTCCTGAAC TTCCAACAAC 400

TGCTCCGAGG AAAGGTGCGT TTCCTGCTCC TTGTAGTGGG GCCCTCCCTC 450
```

-128-

TGTGCCAAGA GGGCCCCACC CGCCATAGCT GTCCCGAGCA GCACCTCTCC 500

ATTCCACACA CTGAACAAGC TCCCAAACAG GACCTCTGGA TTGTTGGAGA 550

CAAACTCCAG TATCTCAGCC AGAACTACTG GCTCTGGATT TCTCAAGAGG 600

CTGCAGGCAT TCAGAGCCAA GATTCCTGGT CTGCTGAACC AAACCTCCAG 650

GTCCCTAGAC CAAATCCCTG GACACCAGAA TGGGACACAC GGACCCTTGA 700

GTGGAATTCA TGGACTCTTT CCTGGACCCC AACCCGGGGC CCTCGGAGCT 750

CCAGACATTC CTCCAGCAAC TTCAGGCATG GGCTCCCGGC CAACCTACCT 800

CCAGCCTGGA GAGTCTCCTT CCCCAGCTCA CCCTTCTCCT GGACGATACA 850

CTCTCTTCTC TCCTTCACCC ACCTCGCCCT CCCCCACAGT CCAGCTCCAG 900

CCTCTGCTTC CTGACCCCTC TGCGATCACA CCCAACTCTA CCAGTCCTCT 950

TCTATTTGCA GCTCACCCTC ATTTCCAGAA CCTGTCTCAG GAAGAGTAAG 1000

GTGCTCAGAC CCTGCCAACT TCAGCA 1026

(2) INFORMATION FOR SEQ ID NO:19:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1014 bases
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AGCCCGGCTC CTCCTGCCTG TGACCCCCGA CTCCTAAATA AACTGCTTCG 50

TGACTCCCAT GTCCTTCACG GCAGACTGAG CCAGTGCCCA GACATTAACC 100

CTTTGTCCAC ACCTGTCCTG CTGCCTGCTG TGGACTTCAC CTTGGGAGAA 150

TGGAAAACCC AGACGGAGCA GACAAAGGCA CAGGATGTCC TGGGAGCCAC 200

AACCCTTCTG CTGGAGGCAG TGATGACAGC ACGGGGACAA GTGGGACCCC 250

CTTGCCTCTC ATCCCTGCTG GTGCAGCTTT CTGGACAGGT TCGCCTCCTC 300

CTCGGGGCCC TGCAGGACCT CCTTGGAATG CAGGGAAGGA CCACAGCTCA 350

CAAGGATCCC AGTGCCATCT TCCTGAACTT CCAACAACTG CTCCGAGGAA 400

AGGTGCGTTT CCTGCTCCTT GTAGTGGGGC CCTCCCTCTG TGCCAAGAGG 450

GCCCCACCCG CCATAGCTGT CCCGAGCAGC ACCTCTCCAT CCACACACT 500

GAACAAGCTC CCAAACAGGA CCTCTGGATT GTTGGAGACA AACTCCAGTA 550

TCTCAGCCAG AACTACTGGC TCTGGATTTC TCAAGAGGCT GCAGGCATTC 600

AGAGCCAAGA TTCCTGGTCT GCTGAACCAA ACCTCCAGGT CCCTAGACCA 650

AATCCCTGGA CACCAGAATG GGACACACGG ACCCTTGAGT GGAATTCATG 700

GACTCTTTCC TGGACCCCAA CCCGGGGCCC TCGGAGCTCC AGACATTCCT 750

CCAGCAACTT CAGGCATGGG CTCCCGGCCA ACCTACCTCC AGCCTGGAGA 800

GTCTCCTTCC CCAGCTCACC CTTCTCCTGG ACGATACACT CTCTTCTCTC 850

CTTCACCCAC CTCGCCCTCC CCCACAGTCC AGCTCCAGCC TCTGCTTCCT 900

GACCCCTCTG CGATCACACC CAACTCTACC AGTCCTCTTC TATTTGCAGC 950

TCACCCTCAT TTCCAGAACC TGTCTCAGGA AGAGTAAGGT GCTCAGACCC 1000

TGCCAACTTC AGCA 1014


(2) INFORMATION FOR SEQ ID NO:20:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 328 amino acids
      (B) TYPE: amino acid
      (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```
Ser Pro Ala Pro Pro Ala Cys Asp Pro Arg Leu Leu Asn Lys Leu
 1               5                  10                  15

Leu Arg Asp Ser His Val Leu His Gly Arg Leu Ser Gln Cys Pro
                20                  25                  30

Asp Ile Asn Pro Leu Ser Thr Pro Val Leu Leu Pro Ala Val Asp
                35                  40                  45

Phe Thr Leu Gly Glu Trp Lys Thr Gln Thr Glu Gln Thr Lys Ala
                50                  55                  60

Gln Asp Val Leu Gly Ala Thr Thr Leu Leu Leu Glu Ala Val Met
                65                  70                  75

Thr Ala Arg Gly Gln Val Gly Pro Pro Cys Leu Ser Ser Leu Leu
                80                  85                  90

Val Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln
                95                  100                 105

Asp Leu Leu Gly Met Gln Gly Arg Thr Thr Ala His Lys Asp Pro
                110                 115                 120

Ser Ala Ile Phe Leu Asn Phe Gln Gln Leu Leu Arg Gly Lys Val
                125                 130                 135

Arg Phe Leu Leu Leu Val Val Gly Pro Ser Leu Cys Ala Lys Arg
                140                 145                 150

Ala Pro Pro Ala Ile Ala Val Pro Ser Ser Thr Ser Pro Phe His
                155                 160                 165

Thr Leu Asn Lys Leu Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr
                170                 175                 180
```

-131-

```
Asn Ser Ser Ile Ser Ala Arg Thr Thr Gly Ser Gly Phe Leu Lys
              185                 190             195

Arg Leu Gln Ala Phe Arg Ala Lys Ile Pro Gly Leu Leu Asn Gln
              200                 205             210

Thr Ser Arg Ser Leu Asp Gln Ile Pro Gly His Gln Asn Gly Thr
              215                 220             225

His Gly Pro Leu Ser Gly Ile His Gly Leu Phe Pro Gly Pro Gln
              230                 235             240

Pro Gly Ala Leu Gly Ala Pro Asp Ile Pro Pro Ala Thr Ser Gly
              245                 250             255

Met Gly Ser Arg Pro Thr Tyr Leu Gln Pro Gly Glu Ser Pro Ser
              260                 265             270

Pro Ala His Pro Ser Pro Gly Arg Tyr Thr Leu Phe Ser Pro Ser
              275                 280             285

Pro Thr Ser Pro Ser Pro Thr Val Gln Leu Gln Pro Leu Leu Pro
              290                 295             300

Asp Pro Ser Ala Ile Thr Pro Asn Ser Thr Ser Pro Leu Leu Phe
              305                 310             315

Ala Ala His Pro His Phe Gln Asn Leu Ser Gln Glu Glu
              320                 325         328
```

(2) INFORMATION FOR SEQ ID NO:21:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 25 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```
Ser Pro Ala Pro Pro Ala Cys Asp Pro Arg Leu Leu Asn Lys Leu
 1               5               10               15

Leu Arg Asp Asp His Val Leu His Gly Arg
              20                  25
```

(2) INFORMATION FOR SEQ ID NO:22:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 27 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

-132-

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```
Ser Pro Ala Pro Pro Ala Cys Asp Pro Arg Leu Leu Asn Lys Leu
1               5               10                  15

Leu Arg Asp Asp His Ser Val Leu His Gly Arg Leu
            20              25      27
```

(2) INFORMATION FOR SEQ ID NO:23:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 25 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

```
Ser Pro Ala Pro Pro Ala Xaa Asp Pro Arg Leu Leu Asn Lys Leu
1               5               10                  15

Leu Arg Asp Asp His Val Leu His Gly Arg
            20              25
```

(2) INFORMATION FOR SEQ ID NO:24:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 14 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```
Xaa Pro Ala Pro Pro Ala Xaa Asp Pro Arg Leu Xaa Asn Lys
1               5               10                  14
```

(2) INFORMATION FOR SEQ ID NO:25:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 9 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```
Pro Arg Leu Leu Asn Lys Leu Leu Arg
1               5               9
```

(2) INFORMATION FOR SEQ ID NO:26:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 45 bases
        (B) TYPE: nucleic acid

```
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:


   GCCGTGAAGG ACGTGGTCGT CACGAAGCAG TTTATTTAGG AGTCG 45



   (2) INFORMATION FOR SEQ ID NO:27:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 20 bases
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:


   CCNGCNCCNC CNGCNTGYGA 20



   (2) INFORMATION FOR SEQ ID NO:28:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 21 bases
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:


   NCCRTGNARN ACRTGRTCRT C 21



   (2) INFORMATION FOR SEQ ID NO:29:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 69 bases
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:


   CCAGCGCCGC CAGCCTGTGA CCCCCGACTC CTAAATAAAC TGCCTCGTGA 50
```

TGACCACGTT CAGCACGGC 69

(2) INFORMATION FOR SEQ ID NO:30:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 69 bases
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:


GCCGTGCTGA ACGTGGTCAT CACGAGGCAG TTTATTTAGG AGTCGGGGGT 50


CACAGGCTGG CGGCGCTGG 69



(2) INFORMATION FOR SEQ ID NO:31:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 69 bases
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:


CCAGCACCTC CGGCATGTGA CCCCCGACTC CTAAATAAAC TGCTTCGTGA 50


CGACCACGTC CATCACGGC 69



(2) INFORMATION FOR SEQ ID NO:32:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 69 bases
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GCCGTGATGG ACGTGGTCGT CACGAAGCAG TTTATTTAGG AGTCGGGGGT 50

CACATGCCGG AGGTGCTGG 69

(2) INFORMATION FOR SEQ ID NO:33:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 69 bases
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CCAGCACCGC CGGCATGTGA CCCCCGACTC CTAAATAAAC TGCTTCGTGA 50

CGATCATGTC TATCACGGT 69

(2) INFORMATION FOR SEQ ID NO:34:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 69 bases
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

ACCGTGATAG ACATGATCGT CACGAAGCAG TTTATTTAGG AGTCGGGGGT 50

CACATGCCGG CGGTGCTGG 69

(2) INFORMATION FOR SEQ ID NO:35:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 37 bases
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GCTAGCTCTA GAAATTGCTC CTCGTGGTCA TGCTTCT 37

(2) INFORMATION FOR SEQ ID NO:36:

   (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 22 bases
(B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CAGTCTGCCG TGAAGGACAT GG 22

(2) INFORMATION FOR SEQ ID NO:37:

   (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 24 bases
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

TGTGGACTTT AGCTTGGGAG AATG 24

(2) INFORMATION FOR SEQ ID NO:38:

   (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 22 bases
(B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GGTCCAGGGA CCTGGAGGTT TG 22

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 31 bases
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
5           (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:


10   ATCGATATCG ATAGCCAGAC ACCCCGGCCA G 31


     (2) INFORMATION FOR SEQ ID NO:40:
15
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 36 bases
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
20          (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:


25   GCTAGCTCTA GACAGGGAAG GGAGCTGTAC ATGAGA 36


     (2) INFORMATION FOR SEQ ID NO:41:
30
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 24 bases
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
35          (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:


40   CTCCTTGGAA CCCAGGGCAG GACC 24


     (2) INFORMATION FOR SEQ ID NO:42:
45
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 24 bases
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
50          (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GGTCCTGCCC TGGGTTCCAA GGAG 24

(2) INFORMATION FOR SEQ ID NO:43:

   (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 27 bases
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTGCTCCGAG GAAAGGACTT CTGGATT 27

(2) INFORMATION FOR SEQ ID NO:44:

   (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 27 bases
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

AATCCAGAAG TCCTTTCCTC GGAGCAG 27

(2) INFORMATION FOR SEQ ID NO:45:

   (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 28 bases
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CCCTCTGCGT CGCGGCGGCC CCACCCAC 28

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 28 bases
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
 5          (D) TOPOLOGY: linear

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:


10   GTGGGTGGGG CCGCCGCGAC GCAGAGGG 28



     (2) INFORMATION FOR SEQ ID NO:47:
15
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 35 bases
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
20          (D) TOPOLOGY: linear

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:


25   GACTCGAGGA TCCATCGATT TTTTTTTTTT TTTTT 35



     (2) INFORMATION FOR SEQ ID NO:48:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 17 bases
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
35          (D) TOPOLOGY: linear

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:


40   GACTCGAGGA TCCATCG 17



     (2) INFORMATION FOR SEQ ID NO:49:
45
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 32 bases
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
50          (D) TOPOLOGY: linear

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

                        -140-

GCTAGCTCTA GAAGCCCGGC TCCTCCTGCC TG 32

(2) INFORMATION FOR SEQ ID NO:50:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21 bases
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:


CGAAATTAAC CCTCACTAAA G 21


(2) INFORMATION FOR SEQ ID NO:51:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 4 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

His Val Leu His
 1           4

(2) INFORMATION FOR SEQ ID NO:52:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 4 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Ser Arg Leu Ser
 1           4

(2) INFORMATION FOR SEQ ID NO:53:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 4 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

-141-

Ser His Val Leu
1           4

(2) INFORMATION FOR SEQ ID NO:54:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 4 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

His Ser Arg Leu
1           4

(2) INFORMATION FOR SEQ ID NO:55:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 4 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Ala Val Asp Phe
1           4

(2) INFORMATION FOR SEQ ID NO:56:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 4 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ser Leu Gly Glu
1           4

(2) INFORMATION FOR SEQ ID NO:57:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 4 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Ala Val Thr Leu
1           4

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 4 amino acids
               (B) TYPE: amino acid
               (D) TOPOLOGY: linear

5
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

     Leu Leu Glu Gly
          1            4
10
     (2) INFORMATION FOR SEQ ID NO:59:

          (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 4 amino acids
15             (B) TYPE: amino acid
               (D) TOPOLOGY: linear

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

20   Leu Ser Ser Leu
          1            4

     (2) INFORMATION FOR SEQ ID NO:60:

          (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 4 amino acids
               (B) TYPE: amino acid
               (D) TOPOLOGY: linear

30        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

     Leu Gly Gln Leu
          1            4

35   (2) INFORMATION FOR SEQ ID NO:61:

          (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 4 amino acids
               (B) TYPE: amino acid
40             (D) TOPOLOGY: linear

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

     Cys Leu Ser Ser
45        1            4

     (2) INFORMATION FOR SEQ ID NO:62:

          (i) SEQUENCE CHARACTERISTICS:
50             (A) LENGTH: 4 amino acids
               (B) TYPE: amino acid
               (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Leu Leu Gly Gln
1        4

(2) INFORMATION FOR SEQ ID NO:63:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 4 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Ser Ser Leu Leu
1        4

(2) INFORMATION FOR SEQ ID NO:64:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 4 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Gly Gln Leu Ser
1        4

(2) INFORMATION FOR SEQ ID NO:65:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 4 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Leu Gln Ser Leu
1        4

(2) INFORMATION FOR SEQ ID NO:66:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 4 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Leu Gly Thr Gln
1        4

-144-

(2) INFORMATION FOR SEQ ID NO:67:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 4 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Ala Leu Gln Ser
1       4

(2) INFORMATION FOR SEQ ID NO:68:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 4 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Leu Leu Gly Thr
1       4

(2) INFORMATION FOR SEQ ID NO:69:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 4 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Asn Ala Ile Phe
1       4

(2) INFORMATION FOR SEQ ID NO:70:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 4 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Leu Ser Phe Gln
1       4

(2) INFORMATION FOR SEQ ID NO:71:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 22 amino acids

(B)  TYPE: amino acid
(D)  TOPOLOGY: linear

(xi)  SEQUENCE DESCRIPTION: SEQ ID NO:71:

Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu
1               5                   10                  15

Leu Arg Asp Ser His Val Leu
                20      22

(2)  INFORMATION FOR SEQ ID NO:72:

    (i)  SEQUENCE CHARACTERISTICS:
        (A)  LENGTH: 24 amino acids
        (B)  TYPE: amino acid
        (D)  TOPOLOGY: linear

    (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:72:

His Ser Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr
1               5                   10                  15

Pro Val Leu Leu Pro Ala Val Asp Phe
                20              24

(2)  INFORMATION FOR SEQ ID NO:73:

    (i)  SEQUENCE CHARACTERISTICS:
        (A)  LENGTH: 23 amino acids
        (B)  TYPE: amino acid
        (D)  TOPOLOGY: linear

    (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:73:

Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln
1               5                   10                  15

Asp Ile Leu Gly Ala Val Thr Leu
                20          23

(2)  INFORMATION FOR SEQ ID NO:74:

    (i)  SEQUENCE CHARACTERISTICS:
        (A)  LENGTH: 21 amino acids
        (B)  TYPE: amino acid
        (D)  TOPOLOGY: linear

    (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:74:

Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Gly Pro Thr
1               5                   10                  15

Cys Leu Ser Ser Leu Leu
                20  21


(2) INFORMATION FOR SEQ ID NO:75:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 16 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Gly Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln
1               5                   10                  15

Ser
16


(2) INFORMATION FOR SEQ ID NO:76:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 22 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Leu Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His
1               5                   10                  15

Lys Asp Pro Asn Ala Ile Phe
                20      22


(2) INFORMATION FOR SEQ ID NO:77:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 25 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met
1               5                   10                  15

Leu Val Gly Gly Ser Thr Leu Cys Val Arg
                20                  25